RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
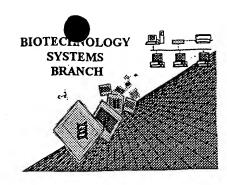BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/506,079C_

Source: _1600_

Date Processed by STIC: _8/14/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/506,079C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino Numbering — The numbering under each 5ᵗʰ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length — Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220> — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (See 1.823 of Sequence Rules)

12 _____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

1600

RAW SEQUENCE LISTING   DATE: 08/14/2001
PATENT APPLICATION: US/09/506,079C   TIME: 16:50:47

Input Set : A:\PTO_VSK.txt
Output Set: N:\CRF3\08142001\I506079C.raw

Does Not Comply
Corrected Diskette Needed

```
  3 <110> APPLICANT: Clinton, Gail M.
  4         Evans, Adam
  5         Henner, William D.
  7 <120> TITLE OF INVENTION: HER-2 BINDING ANTAGONISTS
  9 <130> FILE REFERENCE: 49321-16
 11 <140> CURRENT APPLICATION NUMBER: US 09/506,079C
 12 <141> CURRENT FILING DATE: 2000-02-16
 14 <150> PRIOR APPLICATION NUMBER: US 09/234,208
 15 <151> PRIOR FILING DATE: 1999-01-20
 17 <160> NUMBER OF SEQ ID NOS: 10
```

ERRORED SEQUENCES

```
249 <210> SEQ ID NO: 10
250 <211> LENGTH: 240
251 <212> TYPE: DNA
252 <213> ORGANISM: Homo Sapiens
254 <400> SEQUENCE: 10
255 ggt wcc cac tca cyg cyc ccg agg cca gct gca gtt cct gtc cct  45
256 Gly Xaa His Ser Xaa Xaa Pro Arg Pro Ala Ala Val Pro Val Pro
257                 5                  10                  15
259 cwg cgc atr cag cct gmc cca gcc cac cct gtc cta tcc ttc ctc  90
260 Xaa Arg Xaa Gln Pro Xaa Pro Ala His Pro Val Leu Ser Phe Leu
261                20                  25                  30
263 aga ccc tct tgg gac mta gtc tct gcc ttc tac tct cta ccc ctg 135
264 Arg Pro Ser Trp Asp Xaa Val Ser Ala Phe Tyr Ser Leu Pro Leu
265                35                  40                  45
267 gcc ccc ctc agc cct aca agt gtc cst ata tcc cct gtc agt gtg 180
268 Ala Pro Leu Ser Pro Thr Ser Val Xaa Ile Ser Pro Val Ser Val
269                50                  55                  60
271 ggg agg ggc cyg gac cct gat gct cat gtg gct gtt sac ctg tcc 225
272 Gly Arg Gly Xaa Asp Pro Asp Ala His Val Ala Val Xaa Leu Ser
273                65                  70                  75
275 cgg tat gaa ggc tga                                        240
276 Arg Tyr Glu Gly
286 ⑦
```

see item 9
m Evans
Summary Sheet

E-->
W--> *delete at end of file*

Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

Best Available Copy

VERIFICATION SUMMARY   DATE: 08/14/2001
PATENT APPLICATION: US/09/506,079C   TIME: 16:50:48

Input Set : A:\PTO_VSK.txt
Output Set: N:\CRF3\08142001\I506079C.raw

```
L:12  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:23  M:283 W: Missing Blank Line separator, <220> field identifier
L:27  M:283 W: Missing Blank Line separator, <220> field identifier
L:31  M:283 W: Missing Blank Line separator, <220> field identifier
L:35  M:283 W: Missing Blank Line separator, <220> field identifier
L:39  M:283 W: Missing Blank Line separator, <220> field identifier
L:43  M:283 W: Missing Blank Line separator, <220> field identifier
L:48  M:283 W: Missing Blank Line separator, <220> field identifier
L:52  M:283 W: Missing Blank Line separator, <220> field identifier
L:56  M:283 W: Missing Blank Line separator, <220> field identifier
L:60  M:283 W: Missing Blank Line separator, <220> field identifier
L:66  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:68  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:70  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:72  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:74  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:82  M:283 W: Missing Blank Line separator, <220> field identifier
L:86  M:283 W: Missing Blank Line separator, <220> field identifier
L:90  M:283 W: Missing Blank Line separator, <220> field identifier
L:94  M:283 W: Missing Blank Line separator, <220> field identifier
L:98  M:283 W: Missing Blank Line separator, <220> field identifier
L:102 M:283 W: Missing Blank Line separator, <220> field identifier
L:107 M:283 W: Missing Blank Line separator, <220> field identifier
L:111 M:283 W: Missing Blank Line separator, <220> field identifier
L:115 M:283 W: Missing Blank Line separator, <220> field identifier
L:119 M:283 W: Missing Blank Line separator, <220> field identifier
L:167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:171 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:173 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:175 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:183 M:283 W: Missing Blank Line separator, <220> field identifier
L:193 M:283 W: Missing Blank Line separator, <220> field identifier
L:203 M:283 W: Missing Blank Line separator, <220> field identifier
L:213 M:283 W: Missing Blank Line separator, <220> field identifier
L:223 M:283 W: Missing Blank Line separator, <220> field identifier
L:233 M:283 W: Missing Blank Line separator, <220> field identifier
L:243 M:283 W: Missing Blank Line separator, <220> field identifier
L:256 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10
M:340 Repeated in SeqNo=10
L:286 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
```